APPENDIX 1. DNA analyses support IDs with earthworm biodiversity table at Lake Biwa compared to Samford, Qld. (plus some items of taxonomic "housekeeping").

By Dr R. J. Blakemore, Zama Japan (Feb., 2022).

Regarding the taxa discussed in the current paper: Tissue samples #K2 (*P. bicincta*), #K3-4 (*A. kume*) and #K9 (*M. kinki*) remain at LBM; #K6 *P. bicincta* (KPM-NJL 82) and #K8 *Metaphire kinki* DNA "schiztype" ex Holotype LBM FY2015-8-1 (KPM-NJL 83) are deposited in KPMNH, #K5.2 – *Amynthas kume* tissue sub-sample ex Holotype LBM FY2015-11-1 was resent via KPMNH. Other samples taken for analysis to a lab in India in 2016 all failed. Other results are presented below.

For #K5.1 *Amynthas kume* **Holotype**, an initial gel electrophoresis failed (Fig. 9) but a second attempt of sample #K5.2 with two PCR primers produced a result (Fig. 10).

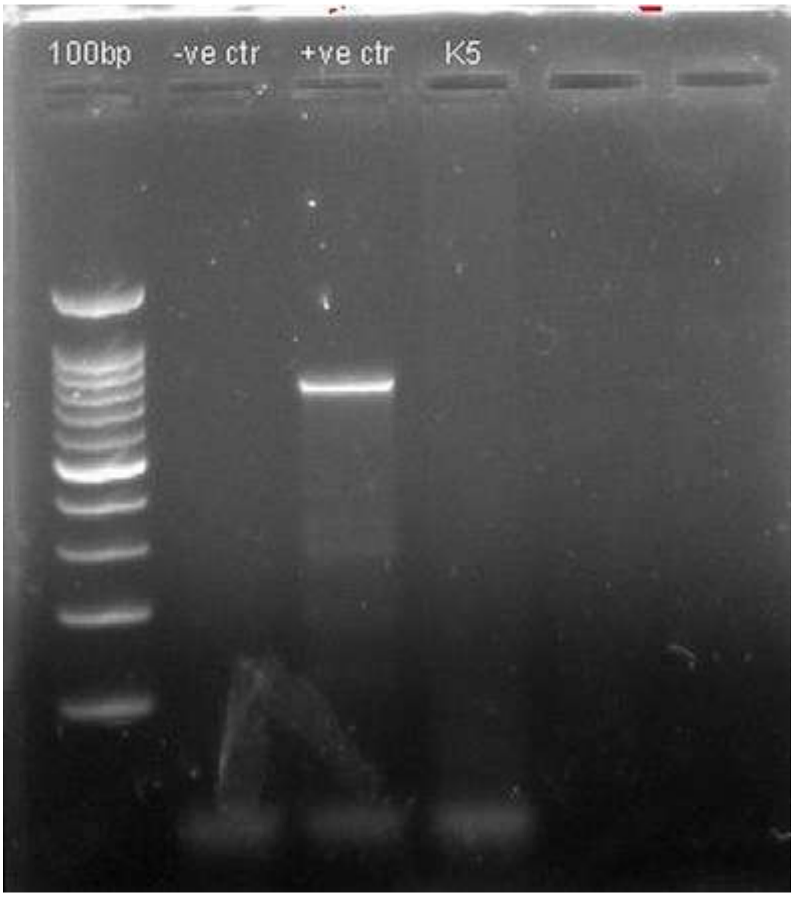

Figure 9. Initial DNA gel image for failed sample #K5.1 that used an original PCR primer set which targets the 900bp COI region (photo from Shu Yong Lim).

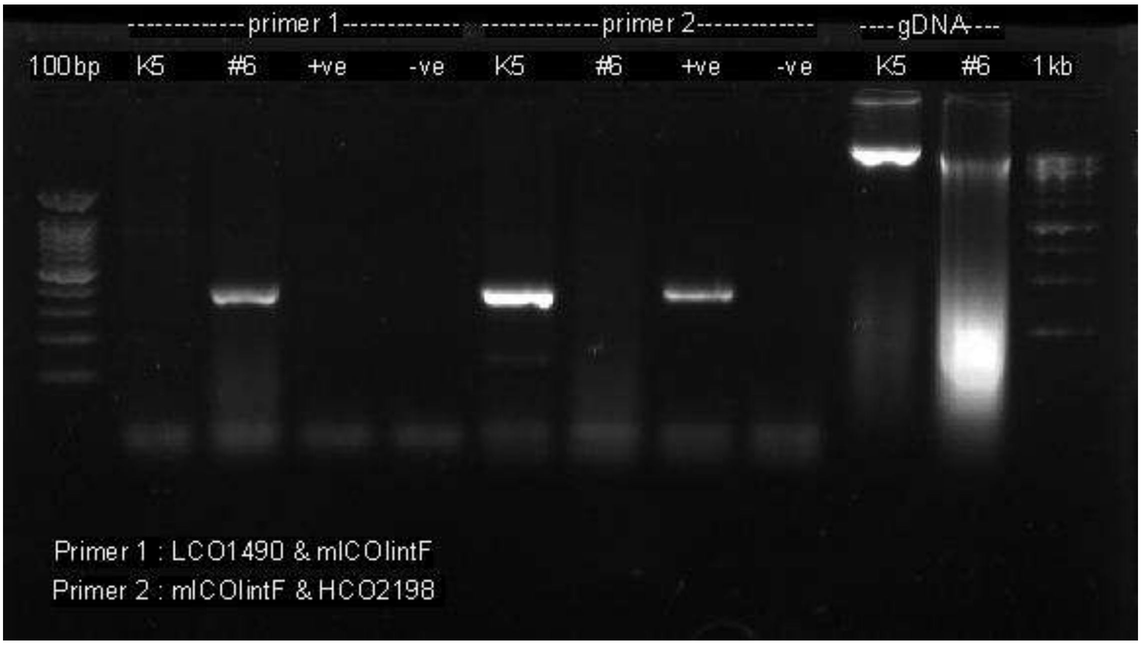
------------primer 1------------
------------primer 2------------
----gDNA---
100bp
K5
#6
+ve
-ve
K5
#6
+ve
-ve
K5
#6
1kb
Primer 1 : LCO1490 & mlCOlintF
Primer 2 : mlCOlintF & HCO2198

Figure 10. mtDNA COI gel image for #K5.2 (*Amynthas kume*) a megascolecid and #6.2 (*Dendrobaena veneta*) a lumbricid when using two different primer sets (photo courtesy of Shu Yong Lim of Monash University Genomics facility, Malaysia).

#3 – *Tokea orthostichon* (Schmarda, 1861) from NZ, tiny tissue sample of Leiden type DNA extraction failed (see Blakemore, 2019b – https://nh.kanagawa-museum.jp/www/contents/1600214845212/simple/bull48_61_68_blakemore.pdf).

#K1 *Amynthas kume* sp. nov. Paratype P1 LBM FY2015-11-2 also failed.

[#K5.1 – *Amynthas kume* sp. nov. Holotype LBM FY2015-11-1 was another failure.
1st_BASE_4320184_K5_LCO1490. First extraction result:
CTTAACAAGGTTACCTTACGGAATTGTGATAACAAAGAACATATAACAAATGAAGA
AGTTAGAGAAAGAACGCTGCTCCCGAGCTTCATACCAAGTTGCCAGAAAGAGAA
GAATTAAATGCGACCGGTACATATACTCAGAATGGAAGAAACAAGAAACCCAAAA
CGAATTTTCAATTACTAACCAGTAAGGGAAAGGGTCTAACGGAAGACCAAAAGGA
TGATGGGTGGACGGATTGGAAGAAGATCTGACCATGGCAAGATTGAGTCTCAATG
GAAAAACTGATGGAAGACACTGACATGACCTTGGAAGAAATAGCAGAAGACAGA
GAACTTTGGAGAAATGTCATGGATAAGTCGATAGCTGGACACAGCTGGAAGACGA
ACACCTGACCTGGCCTGACACTGTGATTGAGAAGCGGGTTACCGTGTGTTGTATC
ACAAATTGGAAATGTTAACTCACATTTTAATCTAAAAATGTTGTTTTGGAAACCGT
GCTGAAACATCCTACTAAATATTGTGCTTATGCTGTAATTTTAACGAGCTTATAAAA

TTTTGGGAAAGAGGGCTGCACAGTATGCAAACTGGGAGGGATCCAGAGGGTAAG
ACAGGGAGAGCATTGGAAAAAGCTGATAATTTTCATTTAACCCCTTTCCTGTGGA
AATGTCTTTTCGAAAACTCCCCACAGACGCTGATTTTTTGGTCACCCTGAAGTTTA
GTCCTAGCTGNTTGCCTGAGA
BLASTn: Query Cover 3%(!). Identity 100.00% KY980442 *Iridomyrmex purpureus* the Australian meat ant (itself likely a misidentification as the ant sample is from USA?). Thus obviously contamination or some other processing error.]

#K5.2 *Amynthas kume* **Holotype** (LBM FY2015-11-1) second attempt:
TAATTGGCGATACTGCCATTGCTGACATCAGTAGACCTTGCAATTTTTTCGCTACA
TTTAGCGGGAGCCTCTTCAATTTTAGGAGCCATTAATTTTATCACCACCGTGATCA
ACATACGTTGATCGGGACTACGTCTAGAACGAATCCCACTATTTGTATGGGCAGT
GGTAATTACCGTAGTACTACTTCTTCTATCCCTACCAGTTTTAGCAGGGGCCATTA
CAATACTATTAACAGACCGAAACCTAAATACTTCATTCTTTGACCCAGCTGGCGGG
GGAGACCCAATTCTATACCAACATCTATTTTGATTTTTTGGTCACCCTGAAGTTTA
GTCATAGCTGTTTCCTGAA
BLASTn: 89.01% *Amynthas yambaruensis* AB542577 from "*Japan:Okinawa, Kunigami village, mt. Yonaha*"; 87.42% "*Amynthas sp.*" KF205397 from China; 86.5% *Amynthas octopapillatus* KF205967 from China. I.e., a new taxon separate by >10.99% difference from any GenBank sequences thus far. Attempts to submit this sequence to Genbank were thwarted with a warning message that the sequences may "*contain internal vector or laboratory adaptor sequence*".

#K7 – *Metaphire kinki* **Holotype** (LBM FY2015-8-1).
TATATATATAATTTTTTACCACTCTTTACTTCTCCTAGGTATCTGACCCGGGATAAT
TGGAGCTGGTATAAGACTATTAATTCGAATTGAATTAAGACAACCGGGCTCATTTT
TAGGAAGTGATCAACTATATAACACAATTGTAACCGCACACGCCTTTCTTATAATC
TTCTTCTTAGTAATACCAGTATTTATTGGAGGATTTGGAAACTGGTTGTTACCTTTA
ATACTTGGAACACCAGACATAGCTTTTCCACGACTTAATAACATAAGATTTTGACT
ACTACCTCCATCGCTTATTCTATTAGTTTCATCTGCTGCAGTAGAAAAAGGAGCTG
GAACAGGATGAACAGTATACCCGCCACTAGCTAGTAATATCGCACATGCTGGACC
CTCCGTAGATCTTGCTATTTTCTCGCTACATTTAGCTGGAGCCTCTTCAATTCTTG
GTGCCATTAATTTCATTACCACAGTAGTTAATATACGATGATCAGGACTACCATTAG
AACGAATTCCACTATTTGTCTGAGCCGTATTAATTACCGTATTACTACTACTACTAT
CCCTACCAGTACTCGCAGGTGCTATTACAATACTACTAACAGACCGTAACCTAAAT
ACATCCTTCTTCGACCCTGCAAGAGGACGATATCCTATCCTATATCTACACCTATC

TTTG

BLASTn: 95.87% AB482078 "*Metaphire sieboldi*" (Horst, 1883) from Nara from: "Minamiya,Y., Yokoyama,J. and Fukuda,T. A phylogeographic study of the Japanese earthworm, *Metaphire sieboldi* (Horst, 1883): Inferences from mitochondrial DNA sequences. *Eur. J. Soil Biol.* 45, 423-430 (2009)".

Although the closest known match, these authors' likely misidentified "*M. sieboldi*" AB482078 from Nara, Kinki (#05 in Group I) differs by 4.13% indicating validity of separation at species level. Other BLASTn matches to their "*M. sieboldi*" were as distant as 12.15% for AB425733 from Aya Town, Kyushu (#21 in Group VI) and up to 14.02% for AB535015 from Umaji Village, Shikoku with other Shikoku samples, e.g. AB607049, AB607069 (Group VII?) about 13.7% different. This confirms that the current sample differs substantially from sequenced specimens attributed to "*M. sieboldi*" sensu lato, the definitive definition of which relies upon eventual DNA sequencing of its Leiden type. Most of their "Groups" are also likely separate taxa.

Summary tables (Tabs. 1–2) are of worm biodiversity at Lake Biwa and at Samford.

Table 1. Update to all worm taxa found at Lake Biwa, Shiga-ken, Kinki, Japan.

	FAMILIES & *Species* of Megadrilacea (i.e., including both Moniligastridae and all other 20 "true worm" families)	**Rice paddy**	**Other habitats**
	MONILIGASTRIDAE		
1	*Drawida eda* Blakemore, 2010 (= "*D.* cf. *barwelli*") **sp. n.***	+	
2	*Drawida hattamimizu* Hatai, 1930*	+	
3	*Drawida japonica* (Michaelsen, 1892) (= "D. *ashiuranoeri*")	+	+
	OCNERODRILIDAE		
4	*Eukerria saltensis* (Beddard, 1895), **new record Kinki**	+	+
	ACANTHODRILIDAE		
5	*Microscolex dubius* (Fletcher, 1887), **new record Asia.**	?	+
6	*Microscolex phosphoreus* (Dugès, 1837), **new record Shiga**	?	+
	MEGASCOLECIDAE *s.* Blakemore, 2000		
7	*Amynthas corticis* (Kinberg, 1867)	+	+
8	*Amynthas carnosus* (Goto & Hatai, 1898) (= "*A. pingi*")	+	+
9	*Amynthas gracilis* (Kinberg, 1867)		+
10	*Amynthas hupeiensis* (Michaelsen, 1895)	+	
11	*Amynthas masatakae* (Beddard, 1892) (= "*A. robustus*")	+?	+
12	*Amynthas megascolidioides* (Goto & Hatai, 1899)*	+	+
13	*Amynthas yamade* Blakemore, 2010, **sp. n. = new species***		+
14	*Metaphire californica* (Kinberg, 1867)		+
15	*Metaphire hilgendorfi* (Michaelsen, 1892)	+	+
16	*Metaphire kinki* Blakemore, 2022, **new species this paper***		+
17	*Metaphire ryunome* Blakemore, 2012, **new species**	+	+
18	? "*Metaphire sieboldi"* (Horst, 1883) (cf. *M. kinki*)*		?+

19	*Metaphire tanbode* Blakemore, 2010, **new species***	+	
20	*Metaphire tosaensis* (Ohfuchi, 1937), **new record Kinki***		+
21	*Metaphire yamadai* (Hatai, 1930), **new record Shiga**		+
	CRIODRILIDAE		
22	*Criodrilus bathybates* Stephenson, 1917*	+	+
	LUMBRICIDAE		
23	*Aporrectodea trapezoides* (Dugès, 1828)	+	+
24	*Bimastos parvus* (Eisen, 1874)	+	+
25	*Dendrodrilus rubidus subrubicundus* (Eisen, 1874)		+
26	*Dendrodrilus rubidus* (Savigny, 1826) (inc. *tenuis* sub-sp?)	+	+
27	*Eisenia anzac* Blakemore, 2011 (sub-sp?), **new for Shiga**		+
28	*Eisenia fetida* (Savigny, 1826) (+ possible sub-spp?)		+
29	*Eisenia japonica* (Michaelsen, 1892) (+ possible sub-spp?)*	+	+
30	*Helodrilus hachiojii* Blakemore, 2007, **new record Shiga***	+	+
	HIRUDINIDAE and all other MICRODRILI Benham, 1890		
31-81+	Leech spp., Enchytraeids + many microdrile spp.**	+	+

* Denotes supposed wholly endemic Japanese megadrile species.

Notes: Due to its disjunct, restricted and mainly coastal distribution, *Drawida hattamimizu* (as described by Blakemore *et al.*, 2010) is here considered likely an introduced taxon from some other Asian country, possibly related to historical piracy raids along Ishikawa/ Fukui coasts. Other Lake Biwa Museum specimens (LBM 1380000087) from Hikone (collected by RJB 18.VI.2009) initially identified as "*Metaphire* spex" or as *A. robustus* (Perrier, 1872) (as *M. masatakae* was then known in 2010), were reallocated to *M. masatakae* by Blakemore (2012a 2020b) and by Blakemore & Lee (2013) or to *Metaphire ryunome* (see Blakemore, 2012a). *Metaphire tosaensis* (Ohfuchi, 1937) specimen in LBM collection from sample #FY2009-10-942 was mislabeled as from landfill around Lake Biwa; actually Nakazono-san collected it from a riverbed in the Suzuka Mts. of Taga-cho near the central eastern borders of Shiga Prefecture just east of Lake Biwa (M.J. Grygier pers. comm. July, 2015). *M. megascolidiodes* (Goto & Hatai, 1899) is described with its DNA barcode published for the first time by Blakemore (2016a). Moreover, several, unidentified, internal nematode parasites were found within the various earthworms inspected, some sent to the Russian Academy for ID.

** Forty-four Microdrile oligochaete taxa were identified by Ohtaka & Nishino (2006), most belonging to the Naididae. In addition to aquatic megadrile *Criodrilus bathybates* (see Blakemore, 2008b), several aquatic microdriles (e.g. *Branchiura* sp., *Tubifex* spp.), enchytraeids (e.g. *Marionina biwaensis* Torii, 2011) and about six species of freshwater leeches (e.g. semi-terrestrial *Odontobdella* cf. *blanchardi* Oka, 1910) were found in the primary author's surveys around the lake. A new record of *Lumbriculus* sp. (possibly *L. variegatus* as found at Mishima), was reported by Blakemore (2016a). However, these groups are not a major interest of import compared to the megadrile (true earthworm) soil fauna.

In following DNA analyses, "JET" code is Japanese Earthworm Taxonomy project (by R. Blakemore, 2010-2011 with iBOLD at Guelph Uni.) and "An-" specimens are in Tokyo National Museum; subsequent codes were miscellaneously generated.

>LK186-187 W4 ***Drawida eda*** **Holotype** CO1 (small letters = single strands):-
atCataaagatattggaacaCTATATTTTATTTTGGGTGTCTGGGCAGGCATAGTTGGAGC
CGGCATAAGGATATTAATTCGTATTGAGCTTAGGCAACCCGGCACATTTTTGGGAA
GAGATCAACTATACAACACTATTGTAACTGCGCATGCTTTTATTATAATTTTCTTTT
TAGTGATGCCTGTGTTTATTGGGGGTTTTGGAAATTGGTTGCTACCTCTGATGCTG
GGAGCACCAGATATAGCTTTTCCCCGTTTAAATAATTTAAGATTTTGATTACTTCCT
CCGGCCCTTATTTTATTAGTTTCTTCTGCTATAGTAGAAAAGGGGGCAGGCACTGG
TTGAACTGTGTATCCTCCCCTAGCTAGTAATATGGCTCACGCAGGTCCTTCTGTTG
ACTTAGCTATTTTTTCCTTGCATTTAGCGGGTGCATCTTCCATTCTAGGATCATTAA
ATTTCATTACCACCGTTATTAATATGCGATGAGTTGGAATGAATATGGAGCGCGTC
CCATTATTTGTATGAGGGGTTTTAATTACTGTAATTCTTTTATTACTATCTTTACCC
GTACTAGCGGGTGCAATCACTATGCTTTTAACAGATCGGAACCTAAATACTTCATT
TTTCGATCCTGCGAGGAGGAGGTGATCCAATTTTATATCAGCACTTATTTTGATTT
TTTGGTCACCCTGAGTTTAA
BLASTn – Dec., 2021: 81.2% KJ782577 *Drawida* sp. from Taiwan, i.e., different taxa.

>GQ500899 *Drawida hattamimizu* (LBM1380000078) **Neotype** from Hatta village.
AGGTGTATGAGCTGGAATAATCGGGGCTGGTATAAGACTTCTTATTCGAATTGAAC
TAAGACAGCCTGGAACATTTTTAGGGAGTGATCAATTATATAATACTATTGTTACA
GCACATGCGTTTATTATAATTTTCTTCTTAGTTATACCAGTATTTATTGGGGGGTTT
GGTAACTGGCTTCTTCCTTTAATACTGGGGGCACCAGATATAGCATTTCCACGACT
TAATAATTTAAGATTTTGATTACTCCCACCATCTTTAATTTTATTAGTTTCCTCAGC
TGCTGTTGAAAAGGGGGCAGGAACAGGTTGAACTGTATACCCCCCATTAGCCAGA
AATATTGCACATGCTGGTCCGTCAGTAGACTTAGCTATTTTTTCTCTTCATTTGGC
AGGTGCCTCATCTATCTTAGGAGCTATTAATTTTATTACAACAGTGATTAATATACG
ATGAGCTGGACTCCAGTTAGAGCGTATTCCACTTTTTGTGTGGGGAGTATTTATCA
CTGTAATTCTTCTTCTTTTATCTCTCCCAGTATTAGCCGGAGCCATTACAATACTAC
TAACAGATCGTAATTTAAATACATCATTTTTTGACCCTGCTGGTGGGGGTGAT

BLASTn Dec., 2021: 100.00% GQ500900, AB543221; 98.86% GQ500901.

>GQ500900 *Drawia hattamimizu* (LBM1380000082) **Topotype**.

> GQ500901 *D. hattamimizu* (LBM1380000084) Shiga-ken, Hikone specimen.

From Blakemore *et al.* (2010): GenBank Accession Nos. were GQ500899-GQ500901 - this the first genetic typification ever for a described earthworm type-specimen - whereas the sequences of the neotype and a topotype agree 100%, the nucleotide bases of a *D. hattamimizu* specimen from Hikone near Lake Biwa differ from these by ca. 1.14%. Since this difference is only slight, all specimens are confirmed as conspecific despite the limited sample. This was the first known sequence for *D. hattamimizu* so, as expected, no correspondence was found from other Internet DNA/RNA sequence searches at that time, subsequently (Dec., 2021) it matches ~100% other *D. hattamimizu* specimens recorded from Japan.

>GQ500902 *Drawida cf. japonica* (LBM1380000085) (see Blakemore & Kupriyanova, 2010; Blakemore *et al.*, 2015)
GAGCTGGAaTAATTGGTGCAGGCATGAGGTTATTAATTCGAATTGAGTTAAGGCA
ACCAGGTTCATTTTTAGGTAGAGATCAGCTTTACAACACTATTGTTACTGCACATG
CTTTTATTATAATTTTTTTCTTGGTAATACCGGTATTTATTGGCGGTTTTGGTAATT
GATTGCTCCCATTAATACTTGGTGCCCCAGATATGGCTTTTCCTCGACTAAATAAT
TTAAGATTTTGACTTTTGCCTCCTGCCCTAATTCTTTTAGTGTCTTCGGCAGCAGT
GGAAAAAGGTGCTGGTACTGGGTGAACAGTTTACCCACCCTTAGCTAGTAATTTA
GCACATGCGGGCCCATCTGTTGACTTGGCGATTTTTTCTTTACATTTAGCAGGTGC
TTCTTCTATTTTAGGGGCAATTAATTTTATTACGACTATTATTAACATGCGCTGAGC
AGGTATACACTTTGAGCGAATTCCATTATTTGTGTGGGGAGTTTTAATTACTGTGG
TACTATTGCTTCTATCTTTACCTGTGTTGGCTGGCGCAATTACTATGCTTTTAACCG
ATCGAAATTTAAATACTTCATTTTTTGATCCGGCTGGTGGAGGAGATC-CTATTT
BLASTn Dec., 2021: 100.0% “Moniligastridae sp.” from China MH845519; 100.0% *Drawida japonica* from Sichuan, China KF205976; (89.8% “*Drawida japonica*” from India MW138943, i.e., >10% different so a likely misidentification from India). Also 100.0% “Drawida ashiuranoeri” MS name from Lake Biwa >JET101-11|LBM FY2010-22.3 & >JET102-11|LBM FY2010-22.4, thus specimens likely = *D. japonica.*

>JET101-11|LBM FY2010-22.3|”Drawida ashiuranoeri”|COI-5P

GACTCTTTATTTTATTTTAGGTGTTTGAGCTGGAATAATTGGTGCAGGCATGAGGT
TATTAATTCGAATTGAGTTAAGGCAACCAGGTTCATTTTTAGGTAGAGATCAGCTT
TACAACACTATTGTTACTGCACATGCTTTTATTATAATTTTTTTCTTGGTAATACCG
GTATTTATTGGCGGTTTTGGTAATTGATTGCTCCCATTAATACTTGGTGCCCCAGA
TATGGCTTTTCCTCGACTAAATAATTTAAGATTTTGACTTTTGCCTCCTGCCCTAAT
TCTTTTAGTGTCTTCGGCAGCAGTGGAAAAAGGTGCTGGTACTGGGTGAACAGTT
TACCCACCCTTAGCTAGTAATTTAGCACATGCGGGCCCATCTGTTGACTTGGCGAT
TTTTTCTTTACATTTAGCAGGTGCTTCTTCTATTTTAGGGGCAATTAATTTTATTAC
GACTATTATTAACATGCGCTGAGCAGGTATACACTTTGAGCGAATTCCATTATTTG
TGTGGGGAGTTTTAATTACTGTGGTACTATTGCTTCTATCTTTACCTGTGTTGGCT
GGCGCAATTACTATGCTTTTAACCGATCGAAATTTAAATACTTCATTTTTTGATCCG
GCTGGTGGAGGAGATCCTATTTTGTATCAACATTTGTTT
BLASTn Dec., 2021: 100.0% *Drawida japonica* from Biwako.

>JET102-11|LBM FY2010-22.4|”Drawida ashiuranoeri”|COI-5P
GACTCTTTATTTTATTTTAGGTGTTTGAGCTGGAATAATTGGTGCAGGCATGAGGT
TATTAATTCGAATTGAGTTAAGGCAACCAGGTTCATTTTTAGGTAGAGATCAGCTT
TACAACACTATTGTTACTGCACATGCTTTTATTATAATTTTTTTCTTGGTAATACCG
GTATTTATTGGCGGTTTTGGTAATTGATTGCTCCCATTAATACTTGGTGCCCCAGA
TATGGCTTTTCCTCGACTAAATAATTTAAGATTTTGACTTTTGCCTCCTGCCCTAAT
TCTTTTAGTGTCTTCGGCAGCAGTGGAAAAAGGTGCTGGTACTGGGTGAACAGTT
TACCCACCCTTAGCTAGTAATTTAGCACATGCGGGCCCATCTGTTGACTTGGCGAT
TTTTTCTTTACATTTAGCAGGTGCTTCTTCTATTTTAGGGGCAATTAATTTTATTAC
GACTATTATTAACATGCGCTGAGCAGGTATACACTTTGAGCGAATTCCATTATTTG
TGTGGGGAGTTTTAATTACTGTGGTACTATTGCTTCTATCTTTACCTGTGTTGGCT
GGCGCAATTACTATGCTTTTAACCGATCGAAATTTAAATACTTCATTTTTTGATCCG
GCTGGTGGAGGAGATCCTATTTTGTATCAACATTTGTTT
BLASTn Dec., 2021: 100.0% >JET101-11 = GQ500902, i.e., same taxon.

>JET128-11|An-468.1|*Eukerria saltensis* from Japan|COI-5P
ATGAGCTGGAATAACAGGTACTGGAATAAGAATAATTATCCGAATCGAACTAAGAC
AGCCAGGCACATTTATAGGGAGGGATCAACTCTACAACACAATTGTAACAGCACA
CGCATTTCTTATAATCTTCTTCCTGGTTATACCAGTTTTTATTGGGGGATTCGGAAA
TTGACTCCTACCACTAATACTTGGTGCTCCTGACATAGCATTCCCTCGACTTAACA
ACATGAGATTCTGACTTCTACCACCGTCCATAACGATCCTAATATTCTCCGCAGCG
GTAGAAAAAGGGGCAGGTACAGGATGAACCCTATACCCCCCCCTCGCTAGAAATA

TAGCACATGCAGGACCATCTGTAGACCTAGCAATCCTATCCCTTCACCTAGCTGG
GGCATCATCAATCCTCGGAGCAATTAACTTTATCACAACAATAATTAATATACGATG
AAATGGAATACGCCTAGAACGTATCCCACTATTTACATGGGCAGTAATAATTACAG
CGATACTCCTTCTACTCTCCCTTCCAGTGCTAGCTGGGGCAATTACCATACTCCTC
ACAGATCGAAATTTAAATACATCATTCTTCGATCCCGCAGGAGGAGGAGATCCAG
TTCTATATCAGCACCTATTC
BLAST nothing better than 80% for *Tonoscolex birmanicus* on Genbank.
11th Nov. 2021 update: 100% MN659344 from NY, USA *Eukerria saltensis*. Q.E.D.

>JET129-11|An-468.2|*Eukerria saltensis* from Japan|COI-5P
TTTAGGAATATGAGCTGGAATAACAGGTACTGGAATAAGAATAATTATCCGAATCG
AACTAAGACAGCCAGGCACATTTATAGGGAGGGATCAACTCTACAACACAATTGT
AACAGCACACGCATTTCTTATAATCTTCTTCCTGGTTATACCAGTTTTTATTGGGG
GATTCGGAAATTGACTCCTACCACTAATACTTGGTGCTCCTGACATAGCATTCCCT
CGACTTAACAACATGAGATTCTGACTTCTACCACCGTCCATAACGATCCTAATATT
CTCCGCAGCGGTAGAAAAAGGGGCAGGTACAGGATGAACCCTATACCCCCCCCTC
GCTAGAAATATAGCACATGCAGGACCATCTGTAGACCTAGCAATCCTATCCCTTCA
CCTAGCTGGGGCATCATCAATCCTCGGAGCAATTAACTTTATCACAACAATAATTA
ATATACGATGAAATGGAATACGCCTAGAACGTATCCCACTATTTACATGGGCAGTA
ATAATTACAGCGATACTCCTTCTACTCTCCCTTCCAGTGCTAGCTGGGGCAATTAC
CATACTCCTCACAGATCGAAATTTAAATACATCATTCTTCGATCCCGCAGGAGGAG
GAGATCCAGTTCTATATCAGCACCTATTC
BLASTn: Jet128 vs JET129 = 634/634 (100%) same taxon.

>JET156-11|An-479|*Microscolex dubius* from Japan|COI-5P
AACACTATACTTCATTTTAGGAGTATGAGCAGGGATAATTGGAGCTGGGATAAGG
CTATTAATCCGTATTGAATTAAGGCAACCCGGGGCATTCCTAGGTAGAGATCAACT
ATATAATACAATTGTTACCGCACATGCATTCTTAATAATTTTTTTCCTGGTAATACC
AGTATTCATTGGAGGATTTGGAAATTGGCTTCTTCCTCTTATATTGGGGGCCCCTG
ACATAGCATTTCCACGACTTAATAATATAAGATTTTGACTGCTACCTCCATCCTTAA
TTCTATTAATTTCATCAGCTGCTGTAGAAAAGGGGGCTGGGACAGGATGAACTGT
ATATCCACCCCTTGCAAGAAATATAGCTCATGCAGGACCATCTGTAGACTTAGCAA
TTTTCTCACTTCATCTTGCAGGAGCCTCGTCCATTTTAGGGGCCATTAACTTTATT
ACTACTGTTGTTAATATACGATCAACAGGTATGCGACTAGAACGAGTACCCTTATT
TGTGTGAGCAGTAATTATTACAGTGGTTCTACTACTTCTTTCTTTACCCGTGTTAG
CTGGAGCCATTACAATACTATTAACTGATCGTAACCTAAATACGTCCTTCTTTGAC

CCTTCAGGTGGTGGAGACCCTATCTTATATCAGCATCTATTC
BLASTn: 615/621 (99%) *Microscolex dubius* JN870091 from "South Africa". Q.E.D.

>JET157-11|An-480|*Microscolex dubius* from Japan|COI-5P
AACACTATACTTCATTTTAGGAGTATGAGCAGGGATAATTGGAGCTGGGATAAGG
CTATTAATCCGTATTGAATTAAGGCAACCCGGGGCATTCCTAGGTAGAGATCAACT
ATATAATACAATTGTTACCGCACATGCATTCTTAATAATTTTTTTCCTGGTAATACC
AGTATTCATTGGAGGATTTGGAAATTGGCTTCTTCCTCTTATATTGGGGGCCCCTG
ACATAGCATTTCCACGACTTAATAATATAAGATTTTGACTGCTACCTCCATCCTTAA
TTCTATTAATTTCATCAGCTGCTGTAGAAAAGGGGGCTGGGACAGGATGAACTGT
ATATCCACCCCTTGCAAGAAATATAGCTCATGCGGGACCATCTGTAGACTTAGCAA
TTTTCTCACTTCATCTTGCAGGAGCCTCGTCCATTTTAGGGGCCATTAACTTTATT
ACTACTGTTGTTAATATACGATCAACAGGTATACGACTAGAACGAGTACCCTTATT
TGTATGAGCAGTAATTATTACAGTGGTTCTACTACTTCTTTCTTTACCCGTGTTAGC
TGGGGCCATTACAATACTATTAACTGATCGTAACCTAAATACCTCCTTCTTTGACC
CTTCAGGTGGTGGAGACCCTATCTTATATCAGCATCTATTC
BLASTn: 620/621(99%) *Microscolex dubius* JN870091 from "South Africa" as above.
BLAST An-479 vs. An-480: 653/658 (99%) thus the two specimens are tolerably same.

For *Microscolex dubius* (Fletcher, 1887), **a new record for Japan and Asia** (see Blakemore, 2012d), the Lake Biwa specimens were from a drain next to bus stop in middle of paddy fields at Kusatsu Shiga-ken, JET-156 and JET-157, in Tokyo Museum An-479 and An-480 collected by RJB 9th August, 2010. Also from paddy drain on walk from Kataoka Ikishira Shrine to the LBM museum, 18th March, 2011 by RJB – single specimen in LBM collection; plus confirmation of *Microscolex phosphoreus* from Japan (Lake Biwa) – collected 18th March, 2011 from drain at Kataoka past bus stop opposite rice paddy by RJB (two specimens in LBM collection).

>JET113-11|An-460.2|"Amynthas cf. pingi"|COI-5P = ***A. carnosus***
AACTTTATATTTTATCTTGGGAATCTGGGCAGGAATAATTGGTGCCGGTATGAGAC
TACTTATTCGAATCGAGCTCAGGCAACCGGGCTCCTTTCTGGGAAGGGACCAACT
ATATAACACAATTGTAACAGCACACGCATTCCTTATAATTTTCTTTCTAGTTATACC
AGTATTCATTGGGGGATTTGGAAATTGGCTACTACCACTCATACTGGGAACACCG
GACATAGCATTTCCACGCCTAAACAACATGAGATTCTGGCTACTGCCCCCATCACT
AATCTTACTAGTATCTTCCGCCGCAGTAGAGAAAGGAGCAGGTACAGGATGAACA
GTATATCCCCCCCTAGCAAGAAATATTGCTCATGCGGGGCCATCAGTAGACCTGG

CAATTTTCTCACTCCACTTAGCTGGGGCATCCTCAATTTTGGGGGCCATTAACTTT
ATTACTACAGTAATTAATATGCGCTGGTCTGGACTACGTCTAGAGCGAATCCCGCT
ATTTGTATGAGCAGTAGTAATTACTGTCGTACTACTATTACTATCATTACCAGTTCT
TGCCGGAGCTATTACAATACTACTAACAGACCGAAACCTAAATACATCATTCTTCG
ACCCAGCGGGAGGGGGGGACCCAATTCTGTACCAACACCTATTT
BLASTn Dec., 2021: 100% KT429008, KP030699 *A. carnosus* from China; 99.84% AB543184 *A. carnosus* from Nara, Japan. Q.E.D. (See Blakemore, 2012e).

>JET114-11|An-461.1|"Amynthas cf. pingi"|COI-5P = ***A. carnosus***
AACTTTATATTTTATCTTGGGAATCTGGGCAGGAATAATTGGTGCCGGTATGAGAC
TACTTATTCGAATCGAGCTCAGGCAACCGGGCTCCTTTCTGGGAAGGGACCAACT
ATATAACACAATTGTAACAGCACACGCATTCCTTATAATTTTCTTTCTAGTTATACC
AGTATTCATTGGGGGATTTGGAAATTGGCTACTACCACTCATACTGGGAACACCG
GACATAGCATTTCCACGCCTAAACAACATGAGATTCTGGCTACTGCCCCCATCACT
AATCTTACTAGTATCTTCCGCCGCAGTAGAGAAAGGAGCAGGTACAGGATGAACA
GTATATCCCCCCCTAGCAAGAAATATTGCTCATGCGGGGCCATCAGTAGACCTGG
CAATTTTCTCACTCCACTTAGCTGGGGCATCCTCAATTTTGGGGGCCATTAACTTT
ATTACTACAGTAATTAATATGCGCTGGTCTGGACTACGTCTAGAGCGAATCCCGCT
ATTTGTATGAGCAGTAGTAATTACTGTCGTACTACTATTACTATCATTACCAGTTCT
TGCCGGAGCTATTACAATACTACTAACAGACCGAAACCTAAATACATCATTCTTCG
ACCCAGCGGGAGGG
BLASTn: JET113 vs. JET114 agree 100%, i.e. same taxon.

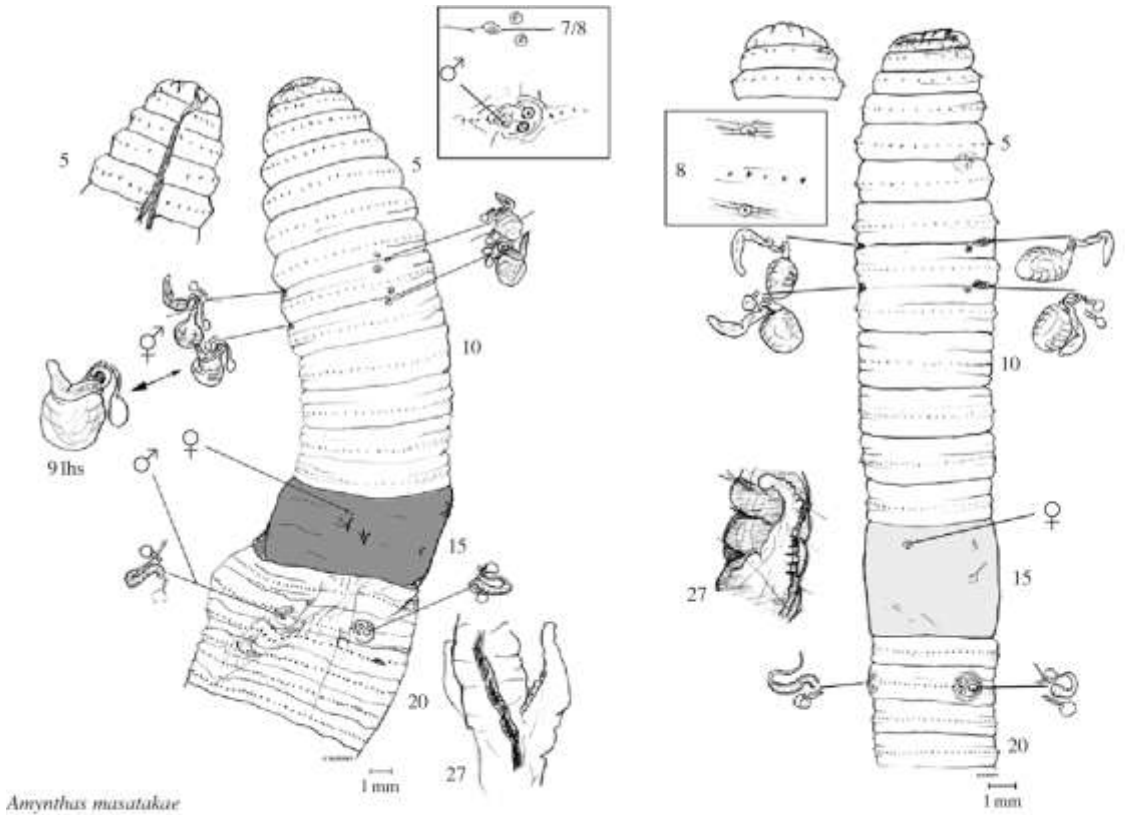

Figure 11. *A. masatakae* lectotype (BMNH1904.5.12-3a) and Nogeyama specimen (NIBR IV0000251098) supplying DNA samples below (from Blakemore, 2012: fig. 1).

>JET032-10 [*Amynthas masatakae*] LECTOTYPE (Blakemore, 2012) [from LONDON type – BMNH1904.5.12-3a] COI partial on first sub-sample [the Sanger generated letter 'N', illustrates ambiguous nucleotide bases that are not deciphered]:
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGGA
GCTATCAACTTCATCACAACAGTAATTAATATACGATGATCTGGATTACGGTTAGA
ACGAATCCCCCTATTCGTCTGAGCAGTAGTTATTACCGTAGTTCTTCTACTCCTTT
CCCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNN
BLAST 2011: Haplotaxida sp. BOLD:AAM4554 voucher 2010GAD-011 cytochrome oxidase, Aug., 2017 & Jan., 2022 ID = 91% “*Amynthas sp.*” from Matsu, Taiwan.
JET032 vs. JET033 = 0.
Jet032 vs. WO35 Nogeyama *A. masatakae* Query cover 15%, ID = 87%, i.e., different taxa? Possibly the old type specimen is contaminated or unreliable due to its age.

>JET033-10 [*Amynthas masatakae*] [BMNH1904.5.12-3b] second sub-sample:
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNCCAGTATTAGCAGGAGCAATTACAATATTAT
TAACAGATCGAAATTTAAATACTTATTTTTTTGACCCTGCTGGAGGAGGAGATCCC
ATTCTTTACCAACATCTATTT
BLAST: Lepidoptera sp. BOLD:AAP4014 = 102/108 (94%), i.e., CONTAMINATION!

>WO35 *A. masatakae* (specimen NIBR IV0000251098) from Nogeyama, Yokohama, Japan collected 4.VI.2012 by RJB & T.J. Tansy (see Blakemore, 2012a, b).
GenBank OM296038 (note GenBank changed my good ID to “*Amythas robustus*”!):
GGAACCTTATACTTTATCCTGGGAATTTGAGCAGGAATAATTGGTGCAGGAATAAG
ACTACTTATTCGTATTGAATTAAGACAACCGGGATCCTTCCTTGGTAGAGACCAAC
TATATAATACAATTGTAACAGCACATGCATTCTTAATAATCTTCTTTCTAGTAATGC
CAGTATTTATTGGTGGATTCGGAAACTGGCTACTGCCCCTAATACTTGGAACCCCA
GATATGGCGTTCCCCCGATTAAATAACATAAGATTTTGACTACTTCCACCATCCCT
AATTTTATTAGTAAGATCGGCCGCGGTAGAAAAAGGAGCGGGCACAGGTTGGACA
GTTTACCCACCCCTAGCAAGAAATATAGCACATGCCGGCCCTTCAGTAGACCTTG
CAATTTTCTCACTCCATCTTGCAGGTGCCTCATCAATTCTTGGAGCTATTAACTTT

ATCACAACAGTAATTAACATGCGATGATCTGGGCTACGTCTAGAACGAATCCCACT
ATTTGTATGAGCAGTAGTGATCACCGTAGTACTATTATTATTATCCCTACCTGTACT
GGCTGGGGCAATTACCATATTACTAACGGATCGAAACCTTAATACATCATTCTTTG
ACCCAGCAGGAGGGGGGGACCCAGTTCTATACCAACACCTATT

BLASTn: 99-100% MH843382 "*Amynthas sp.*" from Sichuan, China; MF541645 "*A. triastrianus*" from "*China, Sichuan*"; AB542533 from Osaka + AB542532 from Tokyo "*A. robustus*" from Japan; EF077575 "*Amynthas hawayanus hawayanus*" from China; or MT444905 "*Amynthas hawayanus*" from North East India (this probably copying the previous misidentified name) – these all misidentifications, as expected.

WO35 vs. w28b Identities = 657/657 (100%), i.e., *A .masatakae* confirmed from Jeju.

WO35 vs. w29 Identities = 614/657 (93%), i.e., different taxa (= *A. tralfamadore*).

WO35 vs. w30 Identities = 617/657 (94%), i.e., different taxa (= *A. tralfamadore*).

WO35 vs. JET032 = 87%, i.e., no match to the lectotype (possibly this classical specimen is too old/contaminated?).

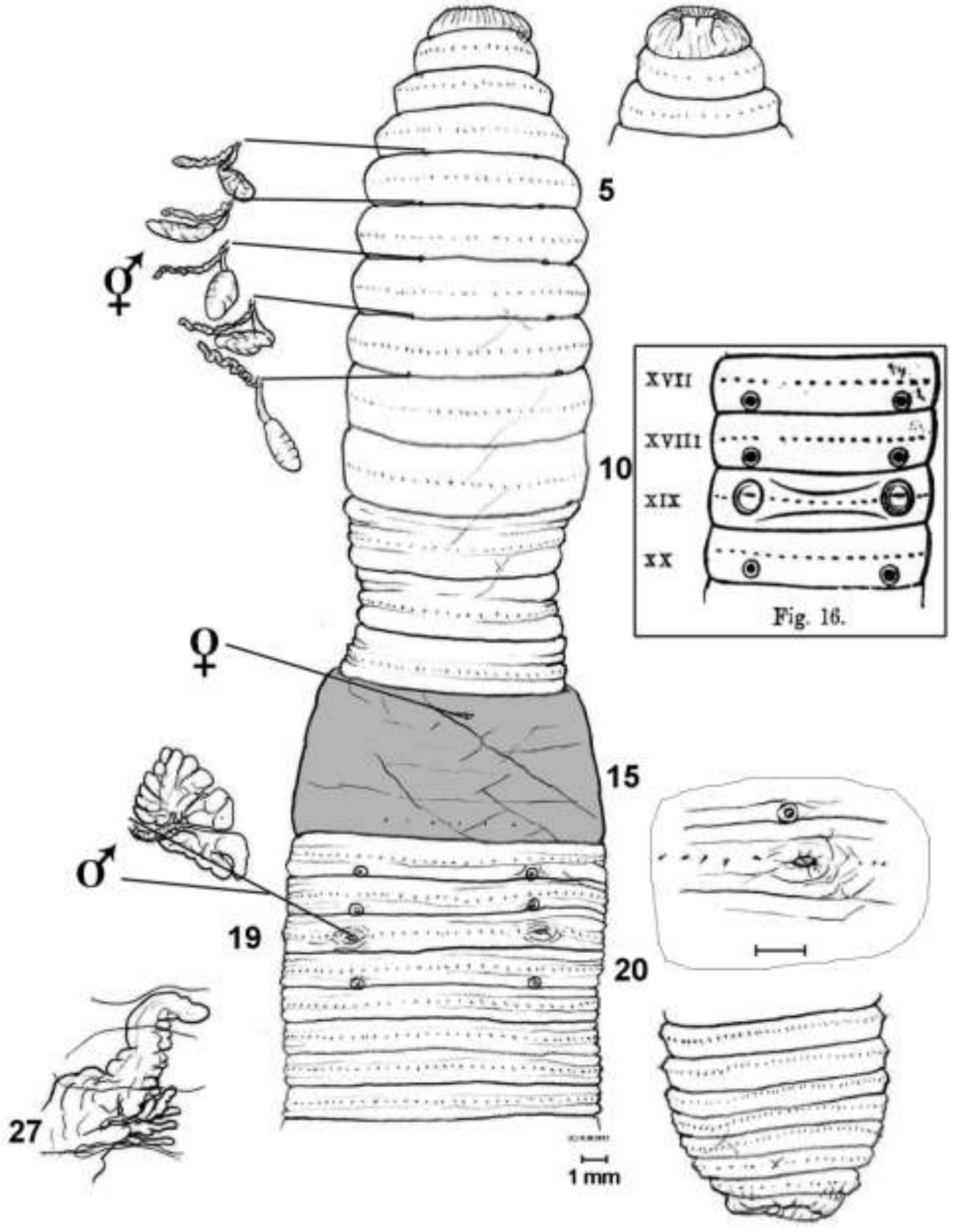

Figure 12. *Metaphire megascolidioides* Nogeyama specimen (coll.: RJB & T.J. Tansey, 3.XII.2011) compared to Goto & Hatai's (1899: fig. 16); DNA data OM296039 below.

>WO37 – *M. megascolidioides* from Nogeyama (RJB + TJT 3.XII.2011) (NIBR IV250896). GenBank OM296039:

ACTTCATTTTAGGAATCTGAGCTGGAATGATTGGGGCAGGAATAAGACTACTCATCCGA
ATTGAACTAAGACAACCAGGTTCATTCTTGGGGAGGGACCAACTATATAATACCATTGT
AACAGCGCACGCATTCCTTATAATTTTCTTTTTAGTAATGCCAGTATTTATTGGGGGATTT

GGAAATTGATTATTACCCCTAATACTAGGAACACCCGATATAGCATTTCCACGACTCAAT
AATATAAGATTTTGACTACTCCCACCATCACTTATTCTTCTAGTATCCTCTGCTGCAGTAG
AAAAAGGAGCAGGAACAGGGTGAACAGTTTATCCTCCCCTAGCAAGAAATATTGCACA
CGCCGGTCCCTCAGTAGACCTTGCAATCTTTTCACTACACCTTGCTGGTGCATCATCAAT
TTTAGGAGCCATTAATTTTATTACCACAGTAATTAATATACGATGATCTGGACTTCGACTA
GAACGAATCCCACTATTCGTCTGAGCAGTAGTGATTACAGTAGTACTGCTATTACTTTCA
CTTCCAGTTCTTGCGGGAGCTATTACAATACTGCTAACAGATCGAAACCTTAATACATCA
TTCTTTGACCCCGCAGGTGGAGGAGACCCAATCCTTTATCAACACCT
BLAST, Jan., 2022: 99.84% LC319410 "Megascolecidae sp." from "Japan: Saga, Sakurei"; 99.5% AB542644 *M. megascolidiodes* from "Japan:Hokkaido, Sapporo city". WO37 vs JET178 *M. megascolidiodes* from Biwako: 99.85%, i.e., same taxon.

>JET178-11|LBM FY2010-22.5|*Metaphire megascolidioides* Biwako specimen-1.
GenBank OM296040:
AACTCTATACTTCATTTTAGGAATCTGAGCTGGAATGATTGGGGCAGGAATAAGAC
TACTCATCCGAATTGAACTAAGACAACCAGGTTCATTCTTGGGGAGGGACCAACT
ATATAATACCATTGTAACAGCACACGCATTCCTTATAATTTTCTTTTTAGTAATGCC
AGTATTTATTGGGGGATTTGGAAATTGATTATTACCCCTAATACTAGGAACACCCG
ATATAGCATTTCCACGACTCAATAATATAAGATTTTGACTACTCCCACCATCACTTA
TTCTTCTAGTATCCTCTGCTGCAGTAGAAAAAGGAGCAGGAACAGGGTGAACAGT
TTATCCTCCCCTAGCAAGAAATATTGCACACGCCGGTCCCTCAGTAGACCTTGCAA
TCTTTTCACTACACCTTGCTGGTGCATCATCAATTTTAGGAGCCATTAATTTTATTA
CCACAGTAATTAATATACGATGATCTGGACTTCGACTAGAACGAATCCCACTATTC
GTCTGAGCAGTAGTGATTACAGTAGTACTGCTATTACTTTCACTTCCAGTTCTTGC
GGGAGCTATTACAATACTGCTAACAGATCGAAACCTTAATACATCATTCTTTGACC
CCGCAGGTGGAGGAGACCCAATCCTTTATCAACACCTGTTT
BLASTn: 99% AB482107 from Kochi, Shikoku & AB542644 from Sapporo, Hokkaido, Japan; but just 92% AB536863 & AB542648 from Fukuoka, Kitakyushu. Difference of these Kyushu specimens of 8% indicate some specific divergence possibly meriting at least sub-specific status; but more work is required to confirm this.

>JET179-11|LBM FY2010-22.6|*Metaphire megascolidioides* Biwako specimen-2.
BLASTn: agrees 100% JET178.

>JET118-11|Tokyo Museum An-463.1| "*Amynthas sp.*"? |COI-5P (a mature specimen from Biwa, collected 2-2-2011 by RJB.

AACACTATACTTCATTTTAGGAATTTGAGCTGGAATAATTGGAGCAGGTATAAGAC
TCCTTATTCGAATTGAACTAAGACAACCGGGCTCATTCCTGGGCAGAGATCAACT
ATATAACACAATTGTCACTGCTCATGCATTCTTAATAATTTTCTTTCTAGTTATACC
AGTATTCATTGGAGGATTTGGAAATTGACTTCTTCCTCTAATACTCGGAACGCCAG
ATATAGCATTCCCACGACTTAATAATATAAGATTTTGACTTTTACCACCCTCTCTAA
TTCTATTAGTATCTTCTGCCGCTGTGGAGAAAGGAGCAGGAACCGGATGAACAGT
ATATCCACCCCTAGCAAGAAATATTGCGCATGCTGGACCATCTGTGGACCTCGCA
ATTTTTTCCCTTCACTTAGCGGGGGCATCATCTATCCTTGGAGCTATCAACTTTATT
ACCACAGTAATTAATATACGTTGATCAGGTCTACGACTAGAACGAATTCCACTATT
TGTATGAGCAGTAGTAATTACTGTAGTCCTACTACTTCTATCCCTACCAGTACTCG
CGGGGGCTATTACAATACTTCTAACAGATCGAAACCTAAATACATCTTTCTTCGAC
CCAGCCGGTGGAGGAGATCCAATTCTATATCAACATCTATTC
BLASTn July, 2016: 100% = *Metaphire yamad*ai (Hatai, 1930) from China KP030697; [also 99.9% *Amynthas pectiniferus* (Michaelsen, 1931) from China KT429018 listed as likely junior synonym in Blakemore (2020a, b)].

>JET119-11|An-463.2|Amynthas sp.|COI-5P
AACACTATACTTCATTTTAGGAATTTGAGCTGGAATAATTGGAGCAGGTATAAGAC
TCCTTATTCGAATTGAACTAAGACAACCGGGCTCATTCCTGGGCAGAGATCAACT
ATATAACACAATTGTCACTGCTCATGCATTCTTAATAATTTTCTTTCTAGTTATACC
AGTATTCATTGGAGGATTTGGAAATTGACTTCTTCCTCTAATACTCGGAACGCCAG
ATATAGCATTCCCACGACTTAATAATATAAGATTTTGACTTTTACCACCCTCTCTAA
TTCTATTAGTATCTTCTGCCGCTGTGGAGAAAGGAGCAGGAACCGGATGAACAGT
ATATCCACCCCTAGCAAGAAATATTGCGCATGCTGGACCATCTGTGGACCTCGCA
ATTTTTTCCCTTCACTTAGCGGGGGCATCATCTATCCTTGGAGCTATCAACTTTATT
ACCACAGTAATTAATATACGTTGATCAGGTCTACGACTAGAACGAATTCCACTATT
TGTATGAGCAGTAGTAATTACTGTAGTCCTACTACTTCTATCCCTACCAGTACTCG
CGGGGGCTATTACAATACTTCTAACAGATCGAAACCTAAATACATCTTTCTTCGAC
CCAGCCGGTGGAGGAGATCCAATTCTATATCAACATCTATTC
BLAST: ditto 100% "Metaphire yamadai".

Hikone *Metaphire ryunome* Holotype (H) An457. BOLD Systems (www.boldsystems.org/) data for holotype tagged An457.1 (compared to sub-samples An457.2 and to paratype (P) An458.1 and An458.2 all initially tagged as “Metaphire robustus” from preliminary identification by RJB).
>JET108-11|An-457.1|”Metaphire cf. robustus”|COI-5P = **Metaphire ryunome H**.

AACTCTATACTTTATTTTAGGAATTTGAGCCGGAATAATCGGAGCTGGGATAAGCC
TACTTATCCGCATTGAACTAAGTCAACCGGGGTCTTTCCTTGGAAGAGACCAGTT
ATATAATACGATTGTAACAGCACATGCATTCCTCATAATTTTCTTCTTAGTAATACC
AGTATTTATTGGGGGGTTCGGAAACTGGTTGCTACCACTAATACTAGGAACACCA
GATATAGCATTCCCCCGACTAAATAACATAAGATTTTGACTACTCCCCCCTTCCCT
AATTCTCCTAGTGAGATCAGCTGCCGTAGAAAAAGGAGCAGGTACAGGTTGAACA
GTATACCCACCCCTAGCAAGAAATATAGCACATGCGGGCCCCTCAGTAGATCTTG
CAATCTTCTCACTACATTTAGCAGGTGCCTCGTCAATTTTAGGAGCTATTAATTTTA
TTACCACAGTGATCAATATACGATGGTCAGGACTACGACTAGAACGAATTCCATTA
TTTGTTTGAGCAGTAATAATTACTGTAGTACTACTACTATTATCACTCCCTGTACTA
GCCGGTGCAATTACTATACTACTAACAGACCGAAATCTTAACACATCCTTCTTTGA
TCCAGCTGGTGGTGGAGACCCAATTCTATACCAACACTTATTC

BLASTn and megaBLAST analyses: An457.1 vs. An457.2 vs. An458.1 vs. An458.2=100%, i.e., specimens same species. Sequence identity of An457.1 with A. *tralfamadore* type is no better than 85%, meaning they are different species. Results of megaBLAST of An457.1 show that it is 99-100% similar to "*Amynthas incongruus*" vouchers EF077552, KF179574 or KP030706 from China and later MT444907 from India; and is just 85% identified with "*Amynthas tristriatus*" voucher EF077538 from China, or with "*Amynthas robustus*" vouchers DQ224191 and AB542533 from Taiwan and Japan, respectively (i.e., similar to *A. tralfamadore* result). However, parthenogenetic *A. incongruus* (Chen, 1933) typically has spermathecal pores in 5/6/7 rather than 7/8/9 and a different arrangement of GMs, at least, compared to those discussed by Blakemore (2012a) for *M. ryunome*. Clearly the identities of the Chinese and (subsequently copied?) Indian specimens are mistakes by amateur taxonomic neophytes that, nevertheless, extend the range of the *M. ryunome* taxon (whatever its taxonomy may ultimately resolve into).

>LK192-193 W5 *Metaphire tanbode* **paratype P7.**

TcataaagatattggaactctatattttattttaggtatctgagctggtataattGGAGCAGGGATAAGACTA
CTTATTCGAATTGAGCTAAGACAACCTGGATCCTTCCTAGGAAGTGATCAACTTTA
TAATACAATTGTAACGGCTCACGCATTCTTGATAATTTTTTTCTTGTAATACCCGT
ATTTATTGGGGGATTTGGAAACTGGTTACTACCCCTTATACTAGGGGCACCAGATA
TAGCATTTCCACGACTCAATAATATAAGATTTTGGTTACTACCCCCTTCCCTTATTT
TATTAGTATCTTCAGCAGCTGTAGAAAAAGGTGCAGGGACAGGGTGAACAGTGTA
TCCACCACTTGCAAGAAATATTGCACATGCTGGCCCCTCCGTAGACCTAGCAATTT
TTTCTCTTCATTTAGCCGGTGCATCATCAATTCTAGGTGCAATTAATTTTATTACTA

CAGTAATCAATATrCGATGGTCTGGACTACGCTTAGAGCGAATCCCGTTATTTGTAT
GAGCAGTTGTAATTACTGTAGTTCTCCTACTTCTATCTCTACCTGTACTAGCCGGT
GCTATTACAATACTACTAACAGATCGAAACCTAAATACATCCTTCTTTGATCCTGCT
GGAGGGGGAGATCCGATTCTATATCAACACTTATTCTGATT
BLASTn Dec., 2021: 89.2% LC573968 *M. hilgendorfi* from Nikko, Tochigi-ken and KX400613 from Kurils, Hokkaido, i.e., substantially different taxa.

>LK172-173 W8 *Metaphire californica* Lake Biwa sample.
atattggaaccttATATTTTATTCTAGGAATCTGAGCAGGGATAATCGGAGCAGGGATAA
GATTACTTATTCGCATCGAACTAAGACAGCCTGGATCATTCCTTGGAAGAGACCA
ACTATATAATACAATTGTGACAGCACACGCATTTCTAATAATTTTCTTTCTGGTGAT
ACCAGTATTTATTGGGGGATTTGGAAACTGACTTCTCCCACTAATGTTAGGAACCC
CTGACATAGCGTTCCCTCGACTAAATAACATAAGATTCTGACTACTGCCACCCTCA
TTAATTCTACTAGTTAGATCCGCGGCAGTAGAAAAGGGAGCAGGTACAGGATGAA
CAGTGTACCCTCCACTAGCTAGAAACATAGCACACGCAGGTCCATCAGTAGATCT
TGCAATTTTCTCACTACATTTAGCAGGTGCCTCATCAATTTTGGGGGCCATCAATT
TCATTACCACTGTGATCAACATGCGATGATCAGGCCTACGCCTAGAGCGAATCCC
ACTATTCGTATGAGCCGTAGTAATCACTGTAGTACTCCTTCTACTATCACTTCCTGT
GCTAGCGGGAGCAATTACTATATTATTAACGGATCGAAACCTAAATACCTCATTCT
TCGACCCTGCAGGTGGGGGAGACCCAATTCTGTATCAACACC
BLASTn Dec., 2021: 100% KX467194 *M. californica* from Shanghai, China. Q.E.D.

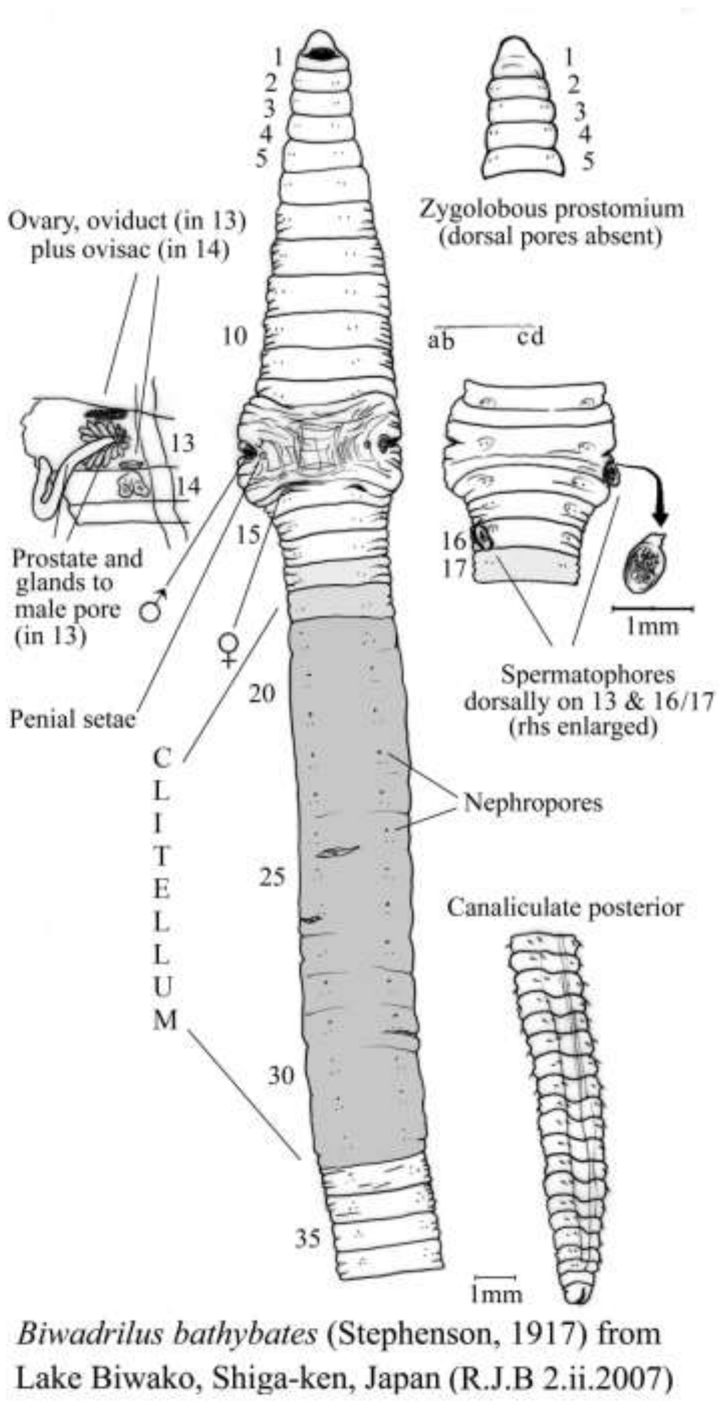

Figure 13. *Criodrilus bathybates* Stephenson, 1917 from Lake Biwako (An-414) collected by RJB providing DNA below (from Blakemore 2008b: fig. 1).

>JET096 | Tokyo Museum specimen An-414.1 | *Criodrilus_bathybates* | **Topotype**.
GenBank OM296041 (note that GenBank changed my ID name!):
AACACTATATTTTATTCTTGGCGTATGAGCGGGAATAATTGGGGCTGGAATAAGCC

TTCTAATTCGAATTGAGCTAAGACAGCCTGGTGCCTTTTTAGGAAGAGACCAACT
TTACAATACCATTGTCACAGCCCATGCTTTCATTATAATTTTCTTTTTAGTGATACC
AGTATTTATCGGGGGATTTGGAAATTGATTACTACCTTTAATACTGGGGGCACCTG
ACATAGCTTTCCCACGATTAAACAATATAAGATTTTGGCTACTACCCCCATCCCTAA
TTCTTTTAGTATCTTCAGCTGCAGTTGAGAAGGGGGCTGGGACTGGATGAACTGT
ATATCCTCCACTTGCCAGAAACTTAGCCCACGGAGGGCCCTCCGTGGATTTAGCA
ATTTTTTCACTTCACTTGGCTGGAGCCTCCTCCATTTTAGGGGCTATCAATTTTATT
ACAACTGTAATTAATATACGATGAAACGGGCTACGCCTAGAGCGAATCCCATTATT
TGTTTGAGCCGTAACCATTACAGTTGTTCTGCTACTTCTATCCCTTCCTGTTCTAG
CTGGAGCCATTACTATGCTATTAACAGACCGAAATCTAAATACATCATTTTTTGAC
CCTGCTGGCGGCGGTGACCCTGTTCTATACCAACACCTATTT
BLASTn 2011 and Dec., 2021: no match topotypic Lake Biwako specimen collected and identified by RJB better than 82% for GU014166 “Glossoscolecidae sp.” [sic] from Brazil (DPEW86596 EW-SJ-867). See Blakemore (2008b).

>JET097-11 Tokyo Museum specimen An-414.2 | *Criodrilus_bathybates* | COI-5P
AACACTATATTTTATTCTTGGCGTATGAGCGGGAATAATTGGGGCTGGAATAAGCC
TTCTAATTCGAATTGAGCTAAGACAGCCTGGTGCCTTTTTAGGAAGAGACCAACT
TTACAATACCATTGTCACAGCCCATGCTTTCATTATAATTTTCTTTTTAGTGATACC
AGTATTTATCGGGGGATTTGGAAATTGATTACTACCTTTAATACTGGGGGCACCTG
ACATAGCTTTCCCACGATTAAACAATATAAGATTTTGGCTACTACCCCCATCCCTAA
TTCTTTTAGTATCTTCAGCTGCAGTTGAGAAGGGGGCTGGGACTGGATGAACTGT
ATATCCTCCACTTGCCAGAAACTTAGCCCACGGAGGGCCCTCCGTGGATTTAGCA
ATTTTTTCACTTCACTTGGCTGGAGCCTCCTCCATTTTAGGGGCTATCAATTTTATT
ACAACTGTAATTAATATACGATGAAACGGGCTACGCCTAGAGCGAATCCCATTATT
TGTTTGAGCCGTAACCATTACAGTTGTTCTGCTACTTCTATCCCTTCCTGTTCTAG
CTGGAGCCATTACTATGCTATTAACAGACCGAAATCTAAATACATCATTTTTTGAC
CCTGCTGGCGGCGGTGACCCTGTTCTATACCAACACCTATTT
BLASTn: JET097 vs. JET096: 100.00% same.

>JET098 | Tokyo Museum specimen An-414.3 | *Criodrilus_bathybates* | COI-5P
AACACTATATTTTATTCTTGGCGTATGAGCAGGAATAATTGGGGCTGGAATAAGCC
TTCTAATTCGAATTGAGCTAAGACAACCTGGTGCCTTTTTAGGAAGAGACCAACT
TTACAATACCATTGTCACAGCCCATGCTTTCATCATAATTTTCTTTTTAGTGATACC
AGTGTTTATCGGGGGATTTGGAAATTGATTACTACCTTTAATACTGGGGGCACCTG
ACATAGCTTTCCCACGATTAAACAATATAAGATTTTGGCTACTGCCCCCATCCCTA

ATTCTTTTAGTATCTTCAGCTGCAGTTGAGAAGGGGGCTGGGACTGGGTGAACTG
TATATCCTCCACTTGCCAGAAACTTAGCCCACGGAGGACCCTCCGTGGATTTAGC
AATTTTTTCACTTCACTTAGCTGGAGCCTCCTCCATTTTAGGGGCTATCAATTTTAT
TACAACTGTAATTAATATACGATGAAACGGGCTACGCCTAGAGCGAATCCCATTAT
TTGTTTGAGCCGTAACCATTACGGTTGTTCTGCTACTTCTATCCCTTCCTGTTCTA
GCTGGAGCCATTACTATGCTATTAACAGACCGAAATCTAAATACATCATTCTTTGA
CCCGGCTGGTGGCGGTGACCCTGTTCTATACCAACACCTATTT
BLASTn: JET096 vs. JET098 646/658 (98%), i.e., slight 2% difference from two samples of topotypic Biwako specimens collected and identified by RJB.

>JET174-11|HNHM-15529|*Eisenia anzac* Blakemore, 2011 **Holotype** from Japan.
AACTTTATATTTTATTCTCGGTGTTTGAGCTGGTATAGTTGGTGCCGGTATAAGA
CTTCTAATTCGAATTGAACTAAGACAGCCGGGAGCCTTCCTAGGAAGAGATCAAC
TATACAATACAATTGTAACAGCTCATGCATTTGTTATAATTTTCTTTTTAGTAATA
CCTGTATTTATTGGGGGATTTGGAAATTGATTACTTCCCCTAATACTAGGAGCCC
CTGACATAGCCTTCCCACGACTAAACAATATAAGATTCTGGTTACTTCCCCCGTC
ACTTATCCTCTTAGTATCTTCCGCTGCTGTAGAAAAAGGTGCAGGTACAGGATGA
ACAGTATACCCCCCCTTATCAAGAAACCTTGCACATGCAGGTCCATCAGTAGATT
TAGCCATCTTTTCTCTTCACCTGGCAGGAGCTTCTTCAATTCTGGGAGCTATTAA
CTTTATCACCACAGTTATCAACATACGTTGAAGAGGATTACGACTAGAACGAATT
CCCCTATTTGTATGAGCTGTAGTTATTACAGTAGTCCTACTTCTTCTATCCCTCCC
AGTGCTCGCAGGAGCCATTACCATGCTACTTACAGATCGAAACTTAAATACTTCA
TTTTTCGACCCTGCCGGTGGTGGAGACCCTATCCTATACCAACATCTTTTC
BLASTn: *E.anzac* vs. *E. j. hiramoto* H Identities = 384/445 (86%) or 4% diferent; *E. anzac* vs. *E. japonica* An-417|Enoshima Japan topotype Identities = 569/658 (86%). JET174 vs. JET099 *E. anzac* from Lake Biwako = 96%, i.e., some 4% divergence.
BLASTn (of type HNHM-15529 from iBOL submission JET174-11 by RJB April, 2011 - http://www.boldsystems.org/views/taxbrowser.php?taxid=315964) – this the first Japanese earthworm Holotype to be simultaneously barcoded) showed greatest similarity (of just ~84%) with two named Genbank lumbricids.

>JET021-10a [organism=*Eisenia anzac*] [HNHM15529 exAn414] COI partial:
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

NNNNNNNNNNNNNNNNATACTAGGAGCCCCTGACATAGCCTTCCCACGACTAA
ACAATATAAGATTCTGGTTACTTCCCCCGTCACTTATCCTCTTAGTATCTTCCGCTG
CTGTAGAAAAAGGTGCAGGTACAGGATGAACAGTATACCCCCCCTTATCAAGAAA
CCTTGCACATGCAGGTCCATCAGTAGATTTAGCCATCTTNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNN
BLASTn: agrees 100% JET0174 *Eisenia anzac* Holotype but only 96% JET099 Biwa specimen, i.e. possibly a separate taxon at specific or sub-specific level.

>JET021-10b [organism=Eisenia anzac] [HNHM15529 exAn414 COI partial
NNNNNNNTATTTTATTCTCGGTGTTTGAGCTGGTATAGTTGGTGCCGGTATAAGA
CTTCTAATTCGAATTGAACTAAGACAGCCGGGAGCCTTCCTAGGAAGNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNGCTTCTTCAATTCTGGGAGCTATTAACTTTATCAC
CACAGTTATCAACATACGTTGAAGAGGATTACGACTAGAACGAATTCCCCTATTTG
TATGAGCTGTAGTTATTACAGTAGTCCTACTTCTTCTATCCCTCCCAGTGCTCGCA
GGAGCCATTACCATGCTACTTACAGATCGAAACTTAAATACTTCATTTTTCGACCC
TGCCGGTGGTGGAGACCCTATNNNNNNNNNNNNNNNNNNN
BLASTn: agrees 100% JET0174 *Eisenia anzac* Holotype; ~95% with JET099 Biwa.

>JET099-11|LBM FY2010-22.1|*Eisenia anzac*|COI-5P
AACTTTATATTTTATTCTCGGTGTTTGAGCTGGTATAGTTGGTGCCGGTATAAGAC
TTCTAATTCGGATTGAACTAAGACAGCCGGGAGCCTTCCTAGGAAGAGATCAACT
ATACAATACAATTGTAACAGCTCACGCATTTGTTATAATTTTCTTTTTAGTAATACC
TGTATTTATCGGAGGATTTGGAAATTGATTACTTCCTCTAATACTAGGAGCCCCTG
ACATAGCCTTCCCACGACTAAACAATATAAGATTCTGATTACTTCCCCCATCACTTA
TCCTCTTAGTATCTTCCGCGGCTGTAGAAAAAGGTGCAGGTACAGGATGAACAGT

ATATCCCCCCCTATCAAGAAACCTTGCACATGCAGGTCCATCAGTAGACCTAGCCA
TCTTTTCTCTTCACTTGGCAGGAGCTTCCTCAATTCTAGGAGCCATTAACTTTATC
ACCACAGTTATCAACATACGTTGAAGAGGGTTACGATTAGAACGAATTCCTTTATT
TGTGTGAGCTGTAGTCATTACAGTAGTCCTACTTCTTCTATCCCTCCCAGTGCTCG
CAGGAGCCATTACCATACTACTTACAGATCGAAACTTAAATACTTCATTTTTCGAC
CCTGCTGGGGGTGGAGACCCTATCCTATATCAACATCTTTTC
BLASTn: JET099 vs JET100 = 100% i.e., same taxon; JET099 vs. JET174 *Eisenia anzac* = 96%, i.e., some divergence. Provisional new name (unpublished) "*Eisenia anzac monax*" [after *Marmota monax* because collected on Groundhog Day (2nd Feb.)].

>JET100-11|LBM FY2010-22.2|*Eisenia anzac*|COI-5P
AACTTTATATTTTATTCTCGGTGTTTGAGCTGGTATAGTTGGTGCCGGTATAAGAC
TTCTAATTCGGATTGAACTAAGACAGCCGGGAGCCTTCCTAGGAAGAGATCAACT
ATACAATACAATTGTAACAGCTCACGCATTTGTTATAATTTTCTTTTTAGTAATACC
TGTATTTATCGGAGGATTTGGAAATTGATTACTTCCTCTAATACTAGGAGCCCCTG
ACATAGCCTTCCCACGACTAAACAATATAAGATTCTGATTACTTCCCCCATCACTTA
TCCTCTTAGTATCTTCCGCGGCTGTAGAAAAAGGTGCAGGTACAGGATGAACAGT
ATATCCCCCCCTATCAAGAAACCTTGCACATGCAGGTCCATCAGTAGACCTAGCCA
TCTTTTCTCTTCACTTGGCAGGAGCTTCCTCAATTCTAGGAGCCATTAACTTTATC
ACCACAGTTATCAACATACGTTGAAGAGGGTTACGATTAGAACGAATTCCTTTATT
TGTGTGAGCTGTAGTCATTACAGTAGTCCTACTTCTTCTATCCCTCCCAGTGCTCG
CAGGAGCCATTACCATACTACTTACAGATCGAAACTTAAATACTTCATTTTTCGAC
CCTGCTGGGGGTGGAGACCCTATCCTATATCAACATCTTTTC

Table 2 Earthworms found on and directly adjacent to a single (ca. 200 ha) mixed/dairy farm at Samford, Queensland (Qld.), Australia (from Blakemore, 1994 - https://espace.library.uq.edu.au/view/UQ:366290/THE8652.pdf with slight updates; most specimens now in ANIC Australian National "Insect" Collection Canberra, ACT).

	FAMILIES and *Species*	**Farm-land**	**Other habitats**
	MONILIGASTRIDAE		
1	*Drawida barwelli* (Beddard, 1886), **new record Australia**	+	
	OCNERODRILIDAE		
2	*Eukerria saltensis* (Beddard, 1895), **new record Qld**	+	+
3	*Ocnerodrilus occidentalis* Eisen, 1878, **new record Qld**	+	
	ACANTHODRILIDAE		
4	*Microscolex phosphoreus* (Dugès, 1837), **new record Qld**	+	
	OCTOCHAETIDAE *s.* Blakemore, 2000		
5	*Dichogaster bolaui* (Michaelsen, 1891)	+	

6	*Dichogaster saliens* (Beddard, 1893), **new record Qld**	+	
7	*Octochaetona beatrix* (Beddard, 1902), **new record Australia**	+	
	MEGASCOLECIDAE *s.* Blakemore, 2000		
8	*Amynthas corticis* (Kinberg, 1867)	+	
9	*Amynthas gracilis* (Kinberg, 1867)	+	
10	*Amynthas minimus* (Horst, 1893)	+	
11	*Amynthas rodericensis* (Grube, 1879)	+	
12	*Anisochaeta megagaster* (Blakemore, 1997), **new species***	+	
13	*Anisochaeta newcombei* (Beddard,1887)*	+	
14	*Anisochaeta novocombei* (Blakemore, 1997), **new species***	+	
15	*Digaster conforma* Blakemore, 1997, **new species***	+	
16	*Digaster minimus* Jam., 1975*	+	
17	*Heteroporodrilus dioecius*, (Stephenson, 1933)*	+	
18	*Heteroporodrilus oxleyensis*, (Fletcher, 1889)*	+	
19	*Heteroporodrilus tryoni* (Fletcher, 1889)* (Closeburn hillside), **DNA COI data as provided for the first time (below)**		+
20	*Perionyx excavatus* Perrier, 1872 (Closeburn in dry riverbed)		+
21	*Polypheretima taprobanae* (Beddard, 1892)	+	
	LUMBRICIDAE		
22	*Aporrectodea rosea* (Savigny, 1826), **new record Qld**	+	+
23	*Aporrectodea trapezoides* (Dugès, 1828)	+	
24	*Bimastos parvus* (Eisen, 1874), **new record Qld**	+	
	GLOSSOSCOLECIDAE		
25	*Pontoscolex corethrurus* (Müller, 1856)	+	+
	ENCHYTRAEIDAE		
	Several Enchytraeids	+	+

*Denotes supposed wholly endemic spp.

>JET103-11|RJB2010.1|*Heteroporodrilus tryoni*| from Closeburn, Qld. RJB 2010. GenBank OM296037:

AACCCTATACTTTATTTTAGGCGTTTGAGCCGGAATAATTGGAGCCGGAATAAGAC
TCTTAATCCGAATTGAATTAAGTCAACCCGGAGCATTTCTCGGAAGTGATCAATTA
TATAATACAATTGTAACTGCACATGCATTTTTAATAATCTTTTTCTTGGTAATACCA
GTATTTATTGGTGGATTTGGAAATTGACTTTTACCACTTATATTAGGGGCACCAGA
TATAGCATTCCCACGACTAAATAATATAAGATTTTGATTACTACCTCCATCACTAAT
TTTACTAGTGTCATCAGCAGCAGTAGAAAAGGGGGCAGGTACTGGATGAACAGTT
TATCCACCTTTAGCAAGAAATATTGCACACTCAGGACCATCAGTAGATTTAGCAAT
TTTTTCTCTACACCTCGCCGGAGCCTCATCAATTCTAGGGGCAATTAACTTTATTA
CAACCGTTGTGAATATACGATGATCTGGGTTACGTTTAGAACGAATTCCACTATTT
GTATGGGCAGTAGTAATTACAGTAGTACTTCTACTCCTGTCACTACCAGTTCTAGC
AGGAGCAATTACAATATTATTAACAGATCGAAATCTAAACACATCATTTTTTGATCC
GGCTGGTGGGGGAGATCCTATTCTATACCAACATCTATTC

BLASTn: no earthworm matches closer than 86%. Recheck 11th Nov., 2021: ditto.

This initial sequence was published in Blakemore (2016a) with a phylogram of all tested species. A 2nd tissue sample from this species – *Heteroporodilus tryoni* (Fletcher, 1889) – is now deposited in Odawara Museum (KPM NJL 81).

Obligatory routine taxonomic "housekeeping" is required (but seems seldom practiced by responsible authorities), thus a review of *Amynthas daeari* Blakemore, 2013 (www.ncbi.nlm.nih.gov/pmc/articles/PMC3689062/pdf/ZooKeys-307-035.pdf) now shows a close 99% match to a specimen identified as *A. jiriensis* (Song & Paik, 1971) (http://www.koreascience.or.kr/article/JAKO197111919884925.pdf):-
>w53 *Amynthas daeari* Blakemore, 2015 Holotype, NIBR IV0000261261.
CTATATTTCATTTTAGGAATTTGAGCTGGAATAATTGGGGCAGGAATAAGACTGCT
TATTCGAATTGAGCTAAGACAGCCGGGCTCTTTTCTAGGAAGGGATCAACTCTATA
ATACAATTGTAACAGCTCATGCATTTTTAATAATCTTCTTTCTTGTAATACCAGTAT
TTATTGGTGGGTTTGGAAATTGACTTCTACCTCTAATACTAGGTGCCCCAGATATA
GCTTTCCCGCGACTTAACAATATAAGATTCTGATTACTGCCCCCATCACTAATTTTA
CTAGTATCGTCTGCAGCAGTAGAAAAAGGTGCCGGAACAGGATGGACAGTGTACC
CCCCACTTGCGAGAAACATTGCACATGCCGGCCCTTCAGTAGATCTTGCAATTTT
TTCTCTCCATCTAGCCGGAGCATCATCAATTCTCGGTGCCATCAACTTCATTACTA
CCGTAATTAATATACGATGATCTGGGCTACGCTTAGAACGAATTCCTCTATTTGTAT
GAGCAGTTGTAATTACTGTAATTCTTTTACTTCTATCTTTACCAGTCTTAGCCGGT
GCTATTACAATATTACTAACAGACCGAAACCTAAATACATCATTTTTTGATCCAGCG
GGAGGAGGTGATCCAATTCTATATCAACACTTATTT
BLASTn (in 2013) GenBank: KF383293: = 88% *Amynthas tappensis* (AB542547) from Japan, i.e., surely a different species. Now (Sept., 2017–Dec., 2021) = 99% *Amynthas jiriensis* KT783537 from Korea. This requires resolution from types of *A. jiriensis* but it should be noted that the original description of *A. daeari* (see Blakemore *et al.*, 2015) had: "*Intestine. Indeterminate as specimen macerated; caeca ventrally incised from 27.*" Possibly the caeca are classable as manicate & incised as in *A. jiriensis* and, if so, then *A. daeari* would become a potential junior synonym, assuming KT783537 ID is verified to type.